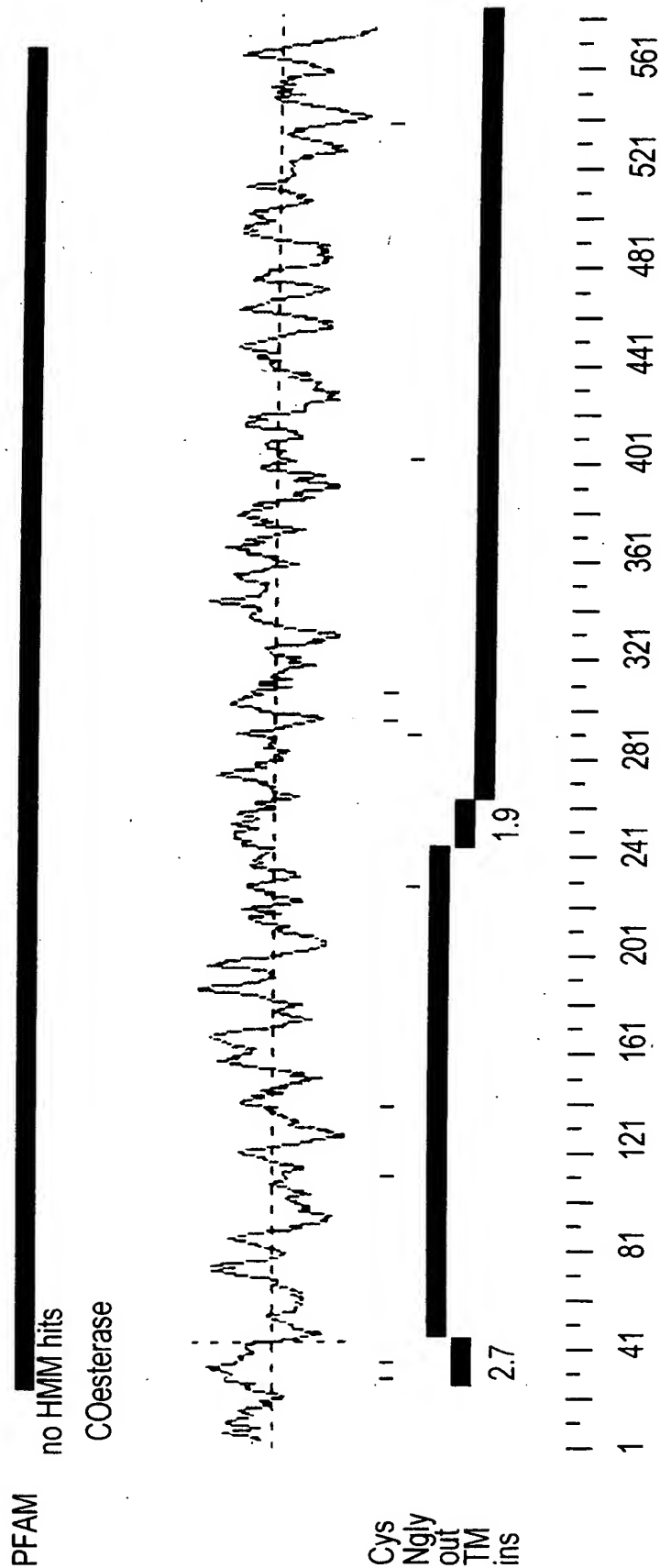FIG. 1

REPLACEMENT SHEET

Applicant: Rosana Kapeller-Libermann, et al.
Title: METHODS OF USING 18903 TO TREAT PAIN AND PAIN-RELATED DISORDERS
Application No.: 10/001,227
Attorney/Agent: Mario Cloutier
Docket No.: MPI00-408P1RM

Sheet 2 of 21 Sheets

FIG. 2A

```
Protein Family / Domain Matches, HMMer version 2

Searching for complete domains in PFAM
hmmpfam - search a single seq against HMM database
HMMER 2.1.1 (Dec 1998)
Copyright (C) 1992-1998 Washington University School of Medicine
HMMER is freely distributed under the GNU General Public License (GPL).
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
HMM file:            /prod/ddm/seqanal/PFAM/pfam6.4/Pfam
Sequence file:       /prod/ddm/wspace/orfanal/oa-script.6214.seq
- - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Query:  Fbh18903FL

Scores for sequence family classification (score includes all domains):
Model       Description                                  Score    E-value  N
--------    -----------                                  -----    -------  -
COesterase  Carboxylesterase                             558.6    4.1e-164 1

Parsed for domains:
Model       Domain  seq-f seq-t    hmm-f hmm-t       score    E-value
--------    ------  ----- -----    ----- -----       -----    -------
COesterase  1/1     25    569 ..    1     612 []      558.6    4.1e-164

Alignments of top-scoring domains:
COesterase: domain 1 of 1, from 25 to 569: score 558.6, E = 4.1e-164
        *->mvllllflllllliavlaaakaspedpllVatnnVlcGkvrGvnek
           +l+ +L l l ++ +l+a+++     ++ V t++   G++ G++
18903  25  RWILCWSLTLCLMAQTALGALHT--KRPQVVTKY--GTLQGKQMH 65

           tdngeqsvysFlGIPYAePPVGnLRFkaPqPYkepWsdvldAtkyppsCl
           +   + +FlG+P+  PP+G LRF +P+P +epW++++dAt+yPP Cl
18903  66  VGKT--PIQVFLGVPFSRPPLGILRFAPPEP-PEPWKGIRDATTYPPGCL 112
```

REPLACEMENT SHEET

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Title: METHODS OF USING 18903 TO TREAT PAIN AND PAIN-RELATED DISORDERS
Application No.: 10/001,227
Attorney/Agent: Mario Cloutier
Docket No.: MPI00-408PIRM

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FIG. 2B

```
18903   113   Qdddfgfslsdlkvalkmlslgwnklvg....lklsEDClYlNVytPknt
                Q + +g+              1 +++ ++ + + 1 +sEDClYlNVy P+ +
18903   113   Q-ESWGQ---------LASMYVSTRErykwLRFSEDCLYLNVYAPARA   150

18903   151   kpnsklPVmVwIhGGGFmfGsghslplslYdgeslaregnVIvVsiNYRL
                + + +lPVmVw +GG+F +G++     s+Y g+ la+++V++V ++ RL
18903   151   PGDPQLPVMVWFPGGAFIVGAA------SSYEGSDLAAREKVVLVFLQHRL   195

18903   196   GplGFLstgddklpgsGNyGLlDQrlALkWvqdNIaaFGGDPnsVTifGe
                G++GFLst+d+++  GN+GLlDQ +AL+WVq+NIaaFGGDP++VT++fG+
18903   196   GIFGFLSTDDSHAR--GNWGLLDQMAALRWVQENIAAFGGDPGNVTLFGQ   243

18903   244   SAGaaSVslllsngGDNppsskgLFhRAIsqSGsalspwaiqsesnarg
                SAGa+S+s l++s   p++ gLFhRAIsqSG+al   +i+s+      +
18903   244   SAGAMSISGLMMS-----PLA-SGLFHRAISQSGTALFRLFITSNP--LK   285

18903   286   rakelarllGCnetssselldClRsksaeeLleatrsfllfeyvpflplf
                ak++a l+GCn++s  l+ ClR  s + + + ++ + f + +f     +
18903   286   VAKKVAHLAGCNHNSTQILVNCLRALSGTKVMRVSNK-MRFlQLNFQRDP   334

18903   335   l....aFgPvvDGdDapeafipedPeelikeGkfadvPyliGvtkdEGgy
                ++  + +PvvDG+     +ip+dP+ 1+ +Gk + vPyl Gv++ E+ +
18903   335   EeiiwSMSPVVDGV-----VIPDDPLVLLTQGKVSSVPYLLGVNNLEFNW   379

18903   380   faamllnasskgedelkketnpdvwlellkyllfyasealnikdMddlad
                ++++ +++ +  + ket ++ 1+   1l+ + +            +
18903   380   LLPYIMKFPLNR-QAMRKETITK-MLWSTRTLlN-ITKEQ--------VP   418

18903   419   kvlekYpgdvddfsvesrkpnlqdmltDllFkcptrvaadlhakhggsPv
                v e+Y++ v  + + ++ + d++ D +F+++  + ++ ++++g Pv
18903   419   LVVEEYlDNVNEHDWKMLRNRMMDIVQDATFVIA-TLQTAHYHRDAGLPV   467
```

REPLACEMENT SHEET

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Application No.: 10/001,227
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Docket No.: MPI00-408P1RM

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FIG. 2C

```
                 YaYvfdhpasfgigQflakrvdpefggavHgdEiffvFgnpllkeqlyka
                 Y+Y+f h+a+      +  v+p+++ga+HgdE+++f+Fg p+ ++ l
18903    468     YLYEFEHHAR-------GIIVKPRTDGADHGDEMYFLFGGPFATG-LS-- 507

                 teeeeksssktmmnywanFAktGnPnngtsnglvvWpkytseeqkYslli
                 e++++s  +mm+YwanFA+tGnP n++  +l+ Wp Y+++e   +l+
18903    508     MGKEKALS-LQMMKYWANFARTGNP-NDG--NLPCWPRYNKDEK--YLQL 551

                 llttitaqklkardprkvlcnfw<-*
                 +tt  +klk+++   ++fw
18903    552     DFTTRVGMKLKEKK-----MAFW      569
```

//
Searching for complete domains in SMART

REPLACEMENT SHEET

Applicant: Rosana Kapeller-Libermann, et al.
Title: METHODS OF USING 18903 TO TREAT PAIN AND PAIN-RELATED DISORDERS
Application No.: 10/001,227
Attorney/Agent: Mario Cloutier
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FIG. 3A

GAP of: FrGcgManager_76_IOA81nWg_ check: 5132 from: 1 to: 1983

Fbh18903FL - Import - vector trimmed

to: FrGcgManager_76_JOA3WXZ1_ check: 1319 from: 1 to: 2456

z34105 in Patent Nucleotide

Symbol comparison table: /ddm_local/gcg/gcg_9.1/
1/gcgcore/data/rundata/nwsgapdna.cmp
CompCheck: 8760


```
        Gap Weight:        12    Average Match: 10.000
     Length Weight:         4    Average Mismatch:  0.000

           Quality:    13796              Length:    2746
             Ratio:    6.957               Gaps:       14
 Percent Similarity:   92.617    Percent Identity: 92.617

     Match display thresholds for the alignment(s):
              | = IDENTITY
              : = 5
              . = 1
```

FrGcgManager_76_IOA81nWg_ x FrGcgManager_76_JOA3WXZ1
..

```
COE-2    1 ...........................................CCT    3

Z34105 101 CATTTCGCCTTGCTGACGGCGTCGAGCCCTGGCCAGACATGTCCACAGGG 150

       4 TTAGCCAATTCGGCCGAGGCCTCCCGCCCCAGTA.CTTGCTGGCAGGGAT  52
          ||  ||   | ||| | |    || ||| | | || || ||
     151 TTCTCCTTCGGGTCCGGGACTCTGGGCTCCACCACCGTGGCCGCCGGCGG 200

      53 TAAGAGCAGA.TAAAAGTGTGCTCACACACTGTAGACACGGCTACCATGC 101
          |  ||||| |     || | |||   |    | ||| ||| || |
     201 GACCAGCACAGGCGGCGTTTTCTCCTTCGGAACGGGAACGTCTAGCAACC 250

     102 CATC.......CACAGTGTTGCCATCCACAGTGTTGCCATCACTCCTGC. 143
          | ||     | ||| | ||| |  |  | |  | ||   |||||  ||
     251 CTTCTGTGGGGCTCAATTTTGGAAATCTTGGAAGTACTTCAACTCCAGCA 300

     144 .CCACAGCAGGAGCT..GGCTGGAGCATGAGGTGGATTCTGTG..CTGGA 188
          | |||| | |   ||     |||   || |  || || ||| ||    |
     301 ACTACATCTGCTCCTTCAAGTGGTTTTGGAACCGGGCTCTTTGGATCTAA 350
```

REPLACEMENT SHEET

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Docket No.: MPI00-408P1RM

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FIG. 3B

```
189  GCCTCACCCT...CTGCCTGATGGCGCAGACGGCCTTGGGTGCCTTGCAC  235
     |||  |  ||      |   ||    || | | ||      |||||||||||||
351  ACCTGCCACTGGGTTCACTCTAGGAGGA.ACAAATACAGGTGCCTTGCAC  399

236  ACCAAGAGGCCTCAAGTGGTCACCAAATATGGAACCCTGCAAGGAAAACA  285
     |||||||||||||||||||||||||||||||||||||||||||||||||
400  ACCAAGAGGCCTCAAGTGGTCACCAAATATGGAACCCTGCAAGGAAAACA  449

286  GATGCATGTGGGGAAGACACCCATCCAAGTCTTTTTAGGAGTCCCCTTCT  335
     |||||||||||||||||||||||||||||||||||||||||||||||||
450  GATGCATGTGGGGAAGACACCCATCCAAGTCTTTTTAGGAGTCCCCTTCT  499

336  CCAGACCTCCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCGGAG  385
     |||||||||||||||||||||||||||||||||||||||||||||||||
500  CCAGACCTCCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCGGAG  549

386  CCCTGGAAAGGAATCAGAGATGCTACCACCTACCCGCCTG..........  425
     ||||||||||||||||||||||||||||||||||||||||
550  CCCTGGAAAGGAATCAGAGATGCTACCACCTACCCGCCTGGATGGAGTCT  599


                                         .
                                         .
                                         .


426  ..........GGTGCCTGCAGGAGTCCTGGGGCCAGCTGGCCTCGATGTA  465
               ||||||||||||||||||||||||||||||||||||||||
700  TGGGGCTACAGGTGCCTGCAGGAGTCCTGGGGCCAGCTGGCCTCGATGTA  749

466  CGTCAGCACGCGGGAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTC  515
     |||||||||||||||||||||||||||||||||||||||||||||||||
750  CGTCAGCACGCGGGAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTC  799

516  TGTACCTGAACGTGTACGCGCCGGCGCGCGCGCCCGGGGATCCCCAGCTG  565
     |||||||||||||||||||||||||||||||||||||||||||||||||
800  TGTACCTGAACGTGTACGCGCCGGCGCGCGCGCCCGGGGATCCCCAGCTG  849

566  CCAGTGATGGTCTGGTTCCCGGGAGGCGCCTTCATCGTGGGCGCTGCTTC  615
     |||||||||||||||||||||||||||||||||||||||||||||||||
850  CCAGTGATGGTCTGGTTCCCGGGAGGCGCCTTCATCGTGGGCGCTGCTTC  899

616  TTCGTACGAGGGCTCTGACTTGGCCGCCCGCGAGAAAGTGGTGCTGGTGT  665
     |||||||||||||||||||||||||||||||||||||||||||||||||
900  TTCGTACGAGGGCTCTGACTTGGCCGCCCGCGAGAAAGTGGTGCTGGTGT  949

666  TTCTGCAGCACAGGCTCGGCATCTTCGGCTTCCTGAGCACGGACGACAGC  715
     |||||||||||||||||||||||||||||||||||||||||||||||||
950  TTCTGCAGCACAGGCTCGGCATCTTCGGCTTCCTGAGCACGGACGACAGC  999

716  CACGCGCGCGGGAACTGGGGGCTGCTGGACCAGATGGCGGCTCTGCGCTG  765
```

FIG. 3C

```
 766  GGTGCAGGAGAACATCGCAGCCTTCGGGGGAGACCCAGGAAATGTGACCC   815
      ||||||||||||||||||||||||||||||||||||||||||||||||||
1050  GGTGCAGGAGAACATCGCAGCCTTCGGGGGAGACCCAGGAAATGTGACCC  1099

 816  TGTTCGGCCAGTCGGCGGGGGCCATGAGCATCTCAGGACTGATGATGTCA   865
      ||||||||||||||||||||||||||||||||||||||||||||||||||
1100  TGTTCGGCCAGTCGGCGGGGGCCATGAGCATCTCAGGACTGATGATGTCA  1149

 866  CCCCTAGCCTCGGGTCTCTTCCATCGGGCCATTTCCCAGAGTGGCACCGC   915
      ||||||||||||||||||||||||||||||||||||||||||||||||||
1150  CCCCTAGCCTCGGGTCTCTTCCATCGGGCCATTTCCCAGAGTGGCACCGC  1199

 916  GTTATTCAGACTTTTCATCACTAGTAACCCACTGAAAGTGGCCAAGAAGG   965
      ||||||||||||||||||||||||||||||||||||||||||||||||||
1200  GTTATTCAGACTTTTCATCACTAGTAACCCACTGAAAGTGGCCAAGAAGG  1249

 966  TTGCCCACCTGGCTGGATGCAACCACAACAGCACACAGATCCTGGTAAAC  1015
      ||||||||||||||||||||||||||||||||||||||||||||||||||
1250  TTGCCCACCTGGCTGGATGCAACCACAACAGCACACAGATCCTGGTAAAC  1299

1016  TGCCTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGAT  1065
      ||||||||||||||||||||||||||||||||||||||||||||||||||
1300  TGCCTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGAT  1349

1066  GAGATTCCTCCAACTGAACTTCCAGAGAGACCCGGAAGAGATTATCTGGT  1115
      ||||||||||||||·|||||||||||||||||||||||||||||||||||
1350  GAGATTCCTCCAACTGAACTTCCAGAGAGACCCGGAAGAGATTATCTGGT  1399

1116  CCATGAGCCCTGTGGTGGATGGTGTGGTGATCCCAGATGACCCTTTGGTG  1165
      ||||||||||||||||||||||||||||||||||||||||||||||||||
1400  CCATGAGCCCTGTGGTGGATGGTGTGGTGATCCCAGATGACCCTTTGGTG  1449

1166  CTCCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTTCTAGGTGTCAA  1215
      ||||||||||||||||||||||||||||||||||||||||||||||||||
1450  CTCCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTTCTAGGTGTCAA  1499

1216  CAACCTGGAATTCAATTGGCTCTTGCCTTATATCATGAAGTTCCCGCTAA  1265
      ||||||||||||||||||||||||||||||||
1500  CAACCTGGAATTCAATTGGCTCTTGCCTTAT....................  1530


                             .

1316  CGCACCCTGTTGAATATCACCAAGGAGCAGGTACCACTTGTGGTGGAGGA  1365
                   |||||||||||||||||||||||||||||||||||||||
1531  ............AATATCACCAAGGAGCAGGTACCACTTGTGGTCGAGGA  1568

1366  GTACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAAACCGTA  1415
```

REPLACEMENT SHEET

Applicant: Rosana Kapeller-Libermann, et al.
Title: METHODS OF USING 18903 TO TREAT PAIN AND PAIN-RELATED
DISORDERS
Application No.: 10/001,227
Attorney/Agent: Mario Cloutier
Docket No.: MPI00-408P1RM
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FIG. 3D

```
1416 TGATGGACATAGTTCAAGATGCCACTTTCGTGTATGCCACACTGCAGACT 1465
     |||||||||||||||||||||||||||||||||||||||||||||||||
1619 TGATGGACATAGTTCAAGATGCCACTTTCGTGTATGCCACACTGCAGACT 1668

1466 GCTCACTACCACCGAGATGCCGGCCTCCCTGTCTACCTGTATGAATTTGA 1515
     ||||||||||||||
1669 GCTCACTACCACCGA............................... 1683




1666 CAACTTTGCCCGCACAGGAAACCCCAATGATGGGAATCTGCCCTGCTGGC 1715
                      |||||||||||||||||||||||||||||||||
1684 ..................GAAACCCCAATGATGGGAATCTGCCCTGCTGGC 1716

1716 CACGCTACAACAAGGATGAAAAGTACCTGCAGCTGGATTTTACCACAAGA 1765
     |||||||||||||||||||||||||||||||||||||||||||||||||
1717 CACGCTACAACAAGGATGAAAAGTACCTGCAGCTGGATTTTACCACAAGA 1766

1766 GTGGGCATGAAGCTCAAGGAGAAGAAGATGGCTTTTTGGATGAGTCTGTA 1815
     |||||||||||||||||||||||||||||||||||||||||||||||||
1767 GTGGGCATGAAGCTCAAGGAGAAGAAGATGGCTTTTTGGATGAGTCTGTA 1816

1816 CCAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGCTATGCA 1865
     |||||||||||||||||||||||||||||||||||||||||||||||||
1817 CCAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGCTATGCA 1866

1866 GGAAGGAGCCAAAGAGGGGTTTGCCCCCACCATCCAGGCCCTGGGGAGAC 1915
     |||||||||||||||||||||||||||||||||||||||||||||||||
1867 GGAAGGAGCCAAAGAGGGGTTTGCCCCCACCATCCAGGCCCTGGGGAGAC 1916

1916 TAGCCATGGACATACCTGGGGACAAGAGTTCTACCCAAGGGCGAATTCGT 1965
     |||||||||||||||||||||||||||||||||||||||   |  |  ||
1917 TAGCCATGGACATACCTGGGGACAAGAGTTCTACCCA...CCCCA...GT 1960

1966 TTAAACCTGCAGGA.CTAG............................. 1983
     ||| | |||||||| ||
1961 TTAGAACTGCAGGAGCTCCCTGCTGCCTCCAGGCCAAAGCTAGAGCTTTT 2010
```

REPLACEMENT SHEET

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Title: METHODS OF USING 18903 TO TREAT PAIN AND PAIN-RELATED DISORDERS
Application No.: 10/001,227
Attorney/Agent: Mario Cloutier
Docket No.: MPI00-408P1RM

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FIG. 4A

```
ALIGN calculates a global alignment of two sequences
version 2.0uPlease cite: Myers and Miller, CABIOS (1989)

                        COE-2   584 aa vs.
                        PRO873  545 aa

scoring matrix: BLOSUM50, gap penalties: -12/-2
62.4% identity;    Global alignment score: 2271

                                                      10
COE-2    M--------------------------------PST-----VLPSTVLPSLLPTAG
          :                                    :: .  . ::  .  . .
pro873   MSTGFSFGSGTLGSTTVAAGGTSTGGVFSFGTGTSSNPSVGLNFGNLGSTSTPATTSAPS
               10        20        30        40        50        60

          20        30        40        50        60        70
COE-2    AGWSMRWILCWSLTLCLMAQTALGALHTKRPQVVTKYGTLQGKQMHVGKTPIQVFLGVPF
          . :: .     .   . :  :::::::::::::::::::::::::::::::::::::::
pro873   SGFGTGLFGSKPATGFTLGGTNTGALHTKRPQVVTKYGTLQGKQMHVGKTPIQVFLGVPF
               70        80        90        100       110       120

          80        90        100       110
COE-2    SRPPLGILRFAPPEPPEPWKGIRDATTYPPG---------------
          ::::::::::::::::::::::::::::::::
pro873   SRPPLGILRFAPPEPPEPWKGIRDATTYPPGWSLALSPGWSAVARSRLTATSASRVQASL
               130       140       150       160       170       180

          120       130       140       150
COE-2    --------------CLQESWGQLASMYVSTRERYKWLRFSEDCLYLNVYAPARAPGDPQLPVM
                        ::::::::::::::::::::::::::::::::::::::::::::::::::
pro873   LPQPLSVWGYRCLQESWGQLASMYVSTRERYKWLRFSEDCLYLNVYAPARAPGDPQLPVM
               190       200       210       220       230       240
```

FIG. 4B

```
          160        170        180        190        200        210
COE-2    VWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLLDQMA
         ::       :: :::::::::::::::::::::::::::::::::::::::::::::::::
pro873   VWFPGGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGFLSTDDSHARGNWGLLDQMA
          250        260        270        280        290        300

          220        230        240        250        260        270
COE-2    ALRWVQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFI
         :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
pro873   ALRWVQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFI
          310        320        330        340        350        360

          280        290        300        310        320        330
COE-2    TSNPLKVAKKVAHLAGCNHNSTQILVNCLRALSGTKVMRVSNKMRFLQLNFQRDPEEIIW
         :::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
pro873   TSNPLKVAKKVAHLAGCNHNSTQILVNCLRALSGTKVMRVSNKMRFLQLNFQRDPEEIIW
          370        380        390        400        410        420

          340        350        360        370        380        390
COE-2    SMSPVVDGVVIPDDPLVLLTQGKVSSSVPYLLGVNNLEFNWLLPYIMKFPLNRQAMRKETI
         ::::::::::::::::::::::::::::::::::::::::        ::
pro873   SMSPVVDGVVIPDDPLVLLTQGKVSSSVPYLLGVNNLEFNWLLPY---------------
          430        440        450        460

          400        410        420        430        440        450
COE-2    TKMLWSTRTLLNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMDIVQDATFVYATLQTAHY
                  :::::::::::::::::::::::::::::::::::::::::::::::: ::::
pro873   ------------NITKEQVPLVVEEYLDNVNEHDWKMLRNRMMDIVQDATFVYATLQTAHY
          470        480        490        500        510
```

FIG. 4C

```
         460        470        480        490        500        510
COE-2    HRDAGLPVYLYEFEHHARGIIVKPRTDGADHGDEMYFLFGGPFATGLSMGKEKALSLQMM
                 ::   : :.       ::   :   : :.
pro873   HRET--PMM-------GIC--P----AGHA--------------------------------
                         520

         520        530        540        550        560        570
COE-2    KYWANFARTGNPNDGNLPCWPRYNKDEKYLQLDFTTRVGMKLKEKKMAFWMSLYQSQRPE
                                      :::.:       :  :.       ::
pro873   --------------------------TTRM------KSTCSWIL-----P-
                                   530                540

         580
COE-2    KQRQF
             :.
pro873   -QEWA
```

REPLACEMENT SHEET

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Application No.: 10/001,227
Attorney/Agent: Mario Cloutier
Docket No.: MPI00-408P1RM

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FIG. 5A
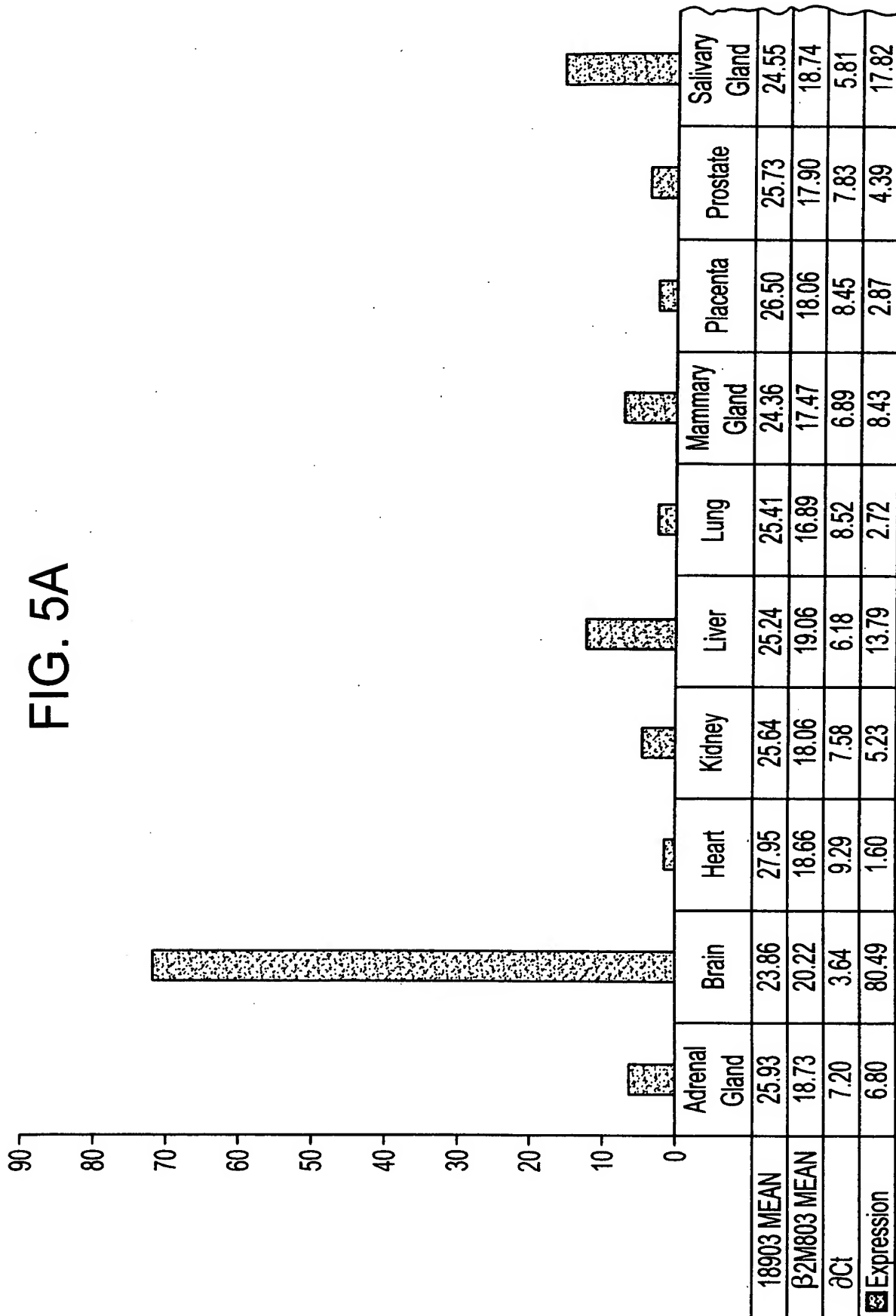
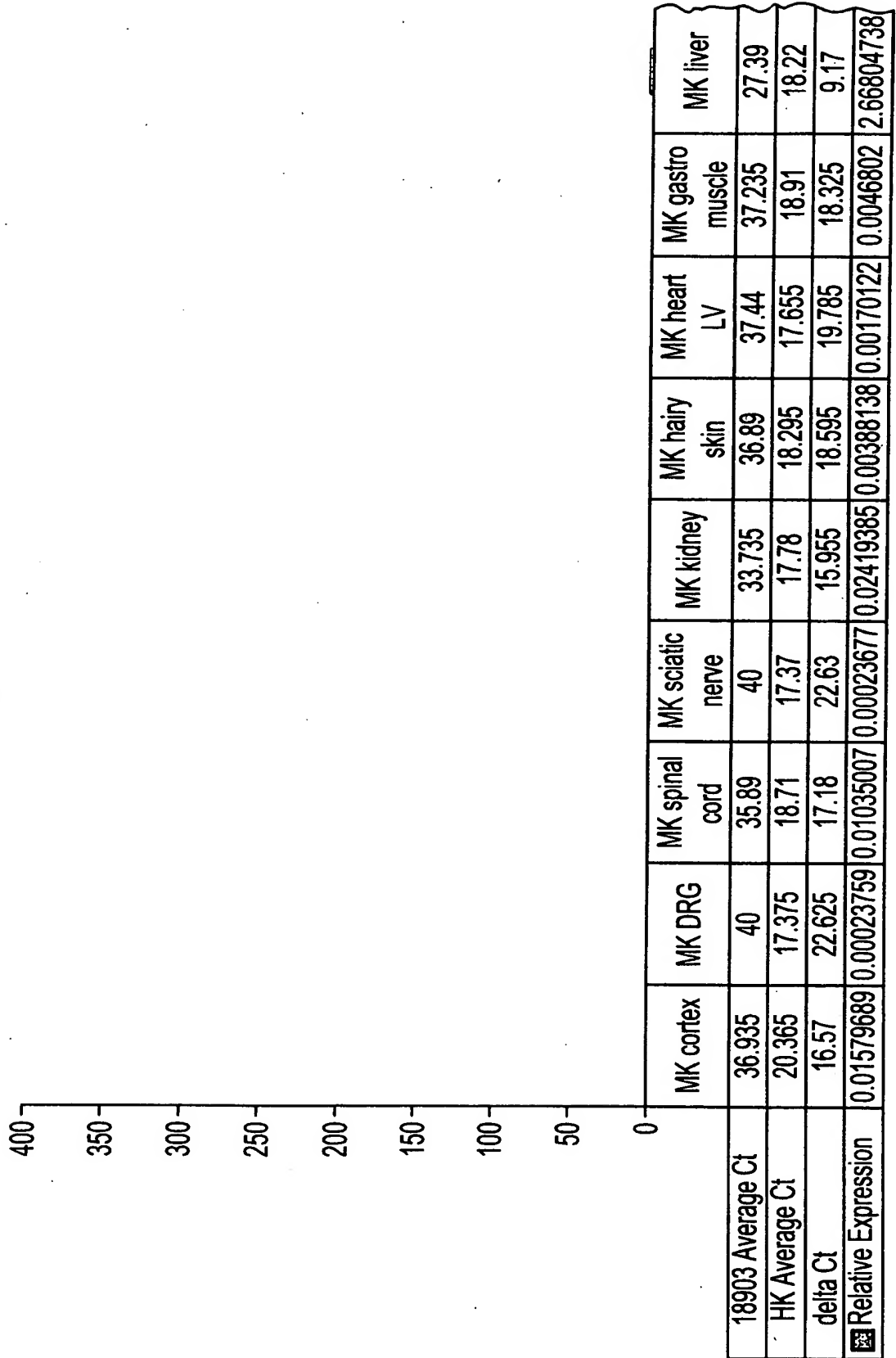|	Adrenal Gland	Brain	Heart	Kidney	Liver	Lung	Mammary Gland	Placenta	Prostate	Salivary Gland
18903 MEAN	25.93	23.86	27.95	25.64	25.24	25.41	24.36	26.50	25.73	24.55
B2M803 MEAN	18.73	20.22	18.66	18.06	19.06	16.89	17.47	18.06	17.90	18.74
∂Ct	7.20	3.64	9.29	7.58	6.18	8.52	6.89	8.45	7.83	5.81
Expression	6.80	80.49	1.60	5.23	13.79	2.72	8.43	2.87	4.39	17.82

REPLACEMENT SHEET

Applicant: Rosana Kapeller-Libermann, et al.
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Application No.: 10/001,227
Attorney/Agent: Mario Cloutier
Docket No.: MP100-408P1RM

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FIG. 5B

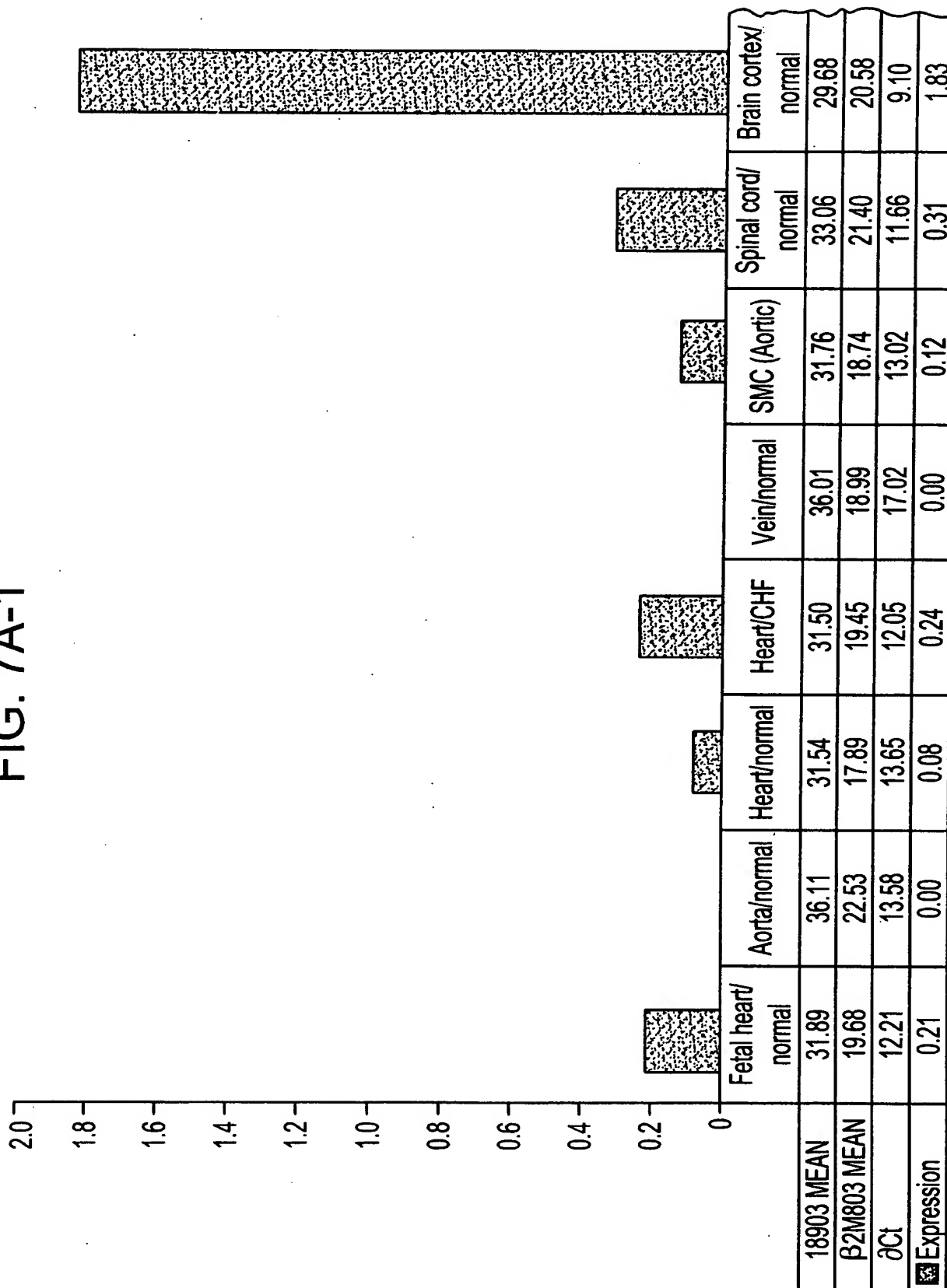| Muscle	Sm. Intestine	Spleen	Stomach	Teste	Thymus	Trachea	Uterus	Spinal Cord	Skin	DRG
29.70	25.43	26.89	26.27	24.29	26.33	25.14	26.18	23.99	23.01	25.06
20.66	17.86	16.37	18.03	19.32	18.19	19.10	18.53	19.20	17.10	19.07
9.04	7.58	10.52	8.25	4.97	8.15	6.04	7.66	4.80	5.91	5.99
1.91	5.24	0.68	3.30	31.91	3.53	15.25	4.96	36.02	16.63	15.73

REPLACEMENT SHEET

Applicant: Rosana Kapeller-Libermann, et al.
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Application No.: 10/001,227
Attorney/Agent: Mario Cloutier
Docket No.: MPI00-408P1RM

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FIG. 6A

	MK cortex	MK DRG	MK spinal cord	MK sciatic nerve	MK kidney	MK hairy skin	MK heart LV	MK gastro muscle	MK liver
18903 Average Ct	36.935	40	35.89	40	33.735	36.89	37.44	37.235	27.39
HK Average Ct	20.365	17.375	18.71	17.37	17.78	18.295	17.655	18.91	18.22
delta Ct	16.57	22.625	17.18	22.63	15.955	18.595	19.785	18.325	9.17
Relative Expression	0.01579689	0.00023759	0.01035007	0.00023677	0.02419385	0.00388138	0.00170122	0.0046802	2.66804738

FIG. 6B

Hu. Brain	Hu. Spinal cord	Hu. Heart	Hu. Kidney	Hu. Liver	Hu. Lung
21.27	23.78	28.26	26.155	25.43	25.805
19.245	18.295	17.855	17.925	18.22	15.87
2.025	5.485	10.405	8.23	7.21	9.935
377.618146	34.3154004	1.13349992	5.11872423	10.3803579	1.57002147

REPLACEMENT SHEET

Applicant: Rosana Kapeller-Libermann, et al.
Title: METHODS OF USING 18903 TO TREAT PAIN AND PAIN-RELATED DISORDERS
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Attorney/Agent: Mario Cloutier
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FIG. 7A-1

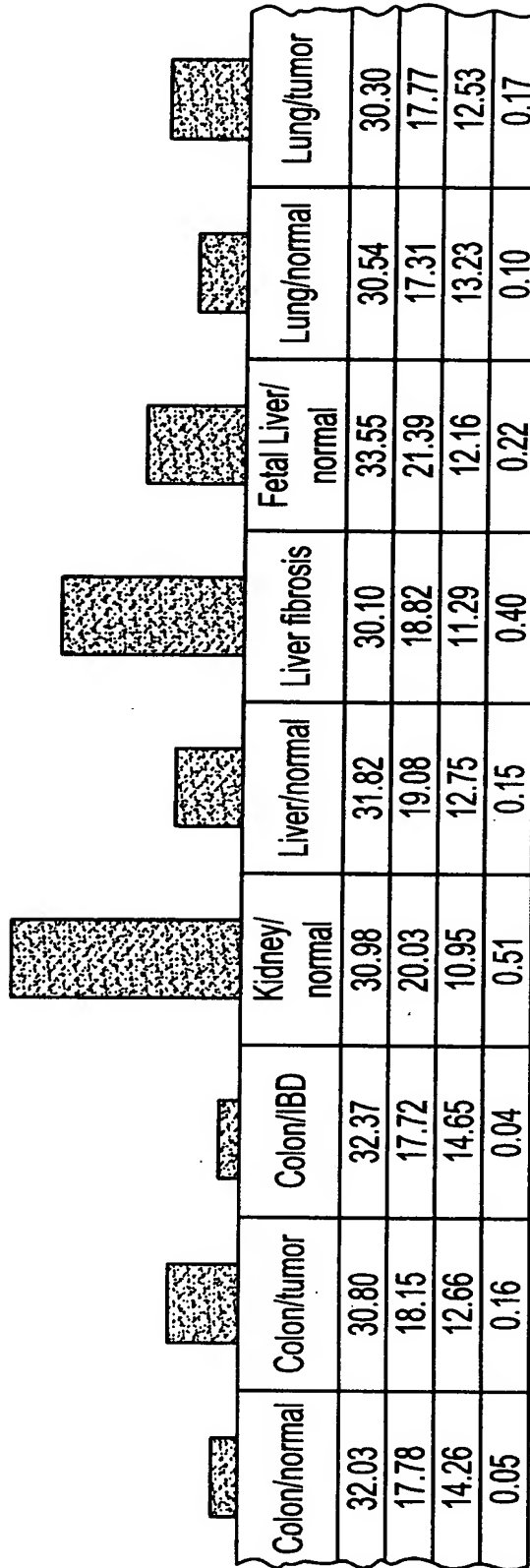|	Fetal heart/ normal	Aorta/normal	Heart/normal	Heart/CHF	Vein/normal	SMC (Aortic)	Spinal cord/ normal	Brain cortex/ normal
18903 MEAN	31.89	36.11	31.54	31.50	36.01	31.76	33.06	29.68
β2M803 MEAN	19.68	22.53	17.89	19.45	18.99	18.74	21.40	20.58
∂Ct	12.21	13.58	13.65	12.05	17.02	13.02	11.66	9.10
Expression	0.21	0.00	0.08	0.24	0.00	0.12	0.31	1.83

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FIG. 7A-2

Brain hypothalamus	Glial cells (Astrocytes)	Brain/ Glioblastoma	Breast/ normal	Breast tumor/ IDC	OVARY/ Normal	OVARY/ Tumor	Pancreas	Prostate/ Normal	Prostate/ Tumor
29.45	33.94	30.39	30.10	30.75	31.73	33.59	30.88	31.16	29.03
19.24	21.09	17.43	18.60	17.66	19.95	18.91	17.33	18.34	17.57
10.21	12.86	12.97	11.50	13.09	11.79	14.68	13.55	12.83	11.46
0.85	0.13	0.13	0.35	0.11	0.28	0.04	0.08	0.14	0.35

REPLACEMENT SHEET

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FIG. 7A-3

Colon/normal	Colon/tumor	Colon/IBD	Kidney/ normal	Liver/normal	Liver fibrosis	Fetal Liver/ normal	Lung/normal	Lung/tumor
32.03	30.80	32.37	30.98	31.82	30.10	33.55	30.54	30.30
17.78	18.15	17.72	20.03	19.08	18.82	21.39	17.31	17.77
14.26	12.66	14.65	10.95	12.75	11.29	12.16	13.23	12.53
0.05	0.16	0.04	0.51	0.15	0.40	0.22	0.10	0.17

FIG. 7A-4

Lung/COPD	Tonsil/normal	Lymph node/normal	Thymus/normal	Epithelial Cells (Prostate)	Endothelial Cells (Aortic)	Skeletal Muscle	Fibroblasts (Dermal)	Skin/Normal	Adipose/Normal
29.44	31.13	-31.40	32.80	30.70	35.27	31.06	33.10	31.16	32.43
17.10	17.19	17.91	20.03	20.13	20.16	18.26	18.18	20.29	17.96
12.34	13.94	13.49	12.78	10.57	15.11	12.81	14.92	10.87	14.47
0.19	0.06	0.09	0.14	0.66	0.03	0.14	0.03	0.54	0.04

REPLACEMENT SHEET

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FIG. 7A-5

Osteoblasts (Primary)	Osteoblasts (Undiff)	Osteoblasts (Diff)	Osteoclasts	Aorta SMC (Early)	Aorta SMC (Late)	HUVEC	HMVEC
34.84	33.19	33.23	32.47	32.50	32.72	32.17	32.74
20.44	18.50	17.83	17.25	19.53	18.77	19.27	18.74
14.40	14.69	15.40	15.22	12.97	13.96	12.91	14.00
0.05	0.04	0.02	0.03	0.13	0.06	0.13	0.06

FIG. 7B

Tissue	18903 MEAN	β2M803 MEAN	δ Ct	Expression
Fetal heart/normal	31.89	19.68	12.21	0.21
Aorta/normal	36.11	22.53	13.58	0.00
Heart normal	31.54	17.89	13.65	0.08
Heart/CHF	31.50	19.45	12.05	0.24
Vein/normal	36.01	18.99	17.02	0.00
SMC (Aortic)	31.76	18.74	13.02	0.12
Spinal cord/normal	33.06	21.40	11.66	0.31
Brain cortex/normal	29.68	20.58	9.10	1.83
Brain hypothalamus/normal	29.45	19.24	10.21	0.85
Glial cells (Astrocytes)	33.94	21.09	12.86	0.13
Brain/Glioblastoma	30.39	17.43	12.97	0.13
Breast/normal	30.10	18.60	11.50	0.35
Breast tumor/IDC	30.75	17.66	13.09	0.11
Ovary/normal	31.73	19.95	11.79	0.28
Ovary/tumor	33.59	18.91	14.68	0.04
Pancreas	30.88	17.33	13.55	0.08
Prostate/normal	31.16	18.34	12.83	0.14
Prostate/tumor	29.03	17.57	11.46	0.35
Colon/normal	32.03	17.78	14.26	0.05
Colon/tumor	30.80	18.15	12.66	0.16
Colon/IBD	32.37	17.72	14.65	0.04
Kidney/normal	30.98	20.03	10.95	0.51
Liver/normal	31.82	19.08	12.75	0.15
Liver/fibrosis	30.10	18.82	11.29	0.40
Fetal Liver/normal	33.55	21.39	12.16	0.22
Lung/normal	30.54	17.31	13.23	0.10
Lung/tumor	30.30	17.77	12.53	0.17
Lung/COPD	29.44	17.10	12.34	0.19
Tonsil/normal	31.13	17.19	13.94	0.06
Lymph node/normal	31.40	17.91	13.49	0.09
Thymus/normal	32.80	20.03	12.78	0.14
Epithelial Cells(prostate)	30.70	20.13	10.57	0.66
Endothelial Cells(aortic)	35.27	20.16	15.11	0.03
Skeletal Muscle/normal	31.06	18.26	12.81	0.14
Fibroblasts (Dermal)	33.10	18.18	14.92	0.03
Skin/normal	31.16	20.29	10.87	0.54
Adipose/normal	32.43	17.96	14.47	0.04
Osteoblasts (primary)	34.84	20.44	14.40	0.05
Osteoblasts (Undiff)	33.19	18.50	14.69	0.04
Osteoblasts (Diff)	33.23	17.83	15.40	0.02
Osteoblasts	32.47	17.25	15.22	0.03
Aorta SMC (Early)	32.50	19.53	12.97	0.13
Aorta SMC (Late)	32.72	18.77	13.96	0.06
HUVEC	32.17	19.27	12.91	0.13
HMVEC	32.74	18.74	14.00	0.06
	40.00	40.00	0.00	